

RAW SEQUENCE LISTING
ERROR REPORT

TECH CENTER 1600/2900

JAN 18 2002

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BIOTECHNOLOGY
SYSTEMS
BRANCH



#18
7/2/02

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/419 901/1641

Source:

O I P E

Date Processed by STIC:

09 18 2001

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NOV 13 2001

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

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Checker Version 3.0

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The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/419901

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/419,901

DATE: 09/18/2001

TIME: 16:19:44

Input Set : A:\Ptq-0021.app

Output Set: N:\CRF3\09182001\I419901.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Van Eyk, Jennifer E
 4 Labugger, Ralf
 5 Neverova, Irena
 7 <120> TITLE OF INVENTION: Methods of Diagnosing Muscle Damage
 9 <130> FILE REFERENCE: 1997-023-04U
 11 <140> CURRENT APPLICATION NUMBER: 09/419,901
 C--> 12 <141> CURRENT FILING DATE: 2001-08-30
 14 <160> NUMBER OF SEQ ID NOS: 7
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 12
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Rattus sp.
 23 <220> FEATURE:
 24 <221> NAME/KEY: UNSURE
 25 <222> LOCATION: (1)..(2)
 27 <220> FEATURE:
 28 <221> NAME/KEY: UNSURE
 29 <222> LOCATION: (7)
 30 <223> OTHER INFORMATION: (P/A) OK
 32 <400> SEQUENCE: 1
 W--> 33 Xaa Xaa Lys Lys Pro Glu Xaa Lys Ala Asp Asp Ala
 34 1 5 10
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 12
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Rattus sp.
 42 <220> FEATURE:
 43 <221> NAME/KEY: UNSURE
 44 <222> LOCATION: (1)
 46 <400> SEQUENCE: 2
 W--> 47 Xaa Pro Ala Pro Ala Ala Pro Ala Ala Pro
 48 1 5 10
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 11
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Rattus sp.
 56 <220> FEATURE:
 57 <221> NAME/KEY: UNSURE
 58 <222> LOCATION: (1)
 60 <220> FEATURE:
 61 <221> NAME/KEY: UNSURE
 62 <222> LOCATION: (8)
 64 <400> SEQUENCE: 3
 W--> 65 Xaa Lys Val Ala Leu Gly Ala Xaa Gly Gly Ile
 66 1 5 10
 69 <210> SEQ ID NO: 4

Errored

FYI: P or A is the preferred format.
 Xaa can only represent a single residue. MH
 When 221 field response is "UNSURE", you must describe the possible amino acids or modified amino acids in field 223.

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/419,901

TIME: 16:19:44

Input Set : A:\Ptq-0021.app

Output Set: N:\CRF3\09182001\I419901.raw

```

70 <211> LENGTH: 13
71 <212> TYPE: PRT
72 <213> ORGANISM: Rattus sp.
74 <220> FEATURE:
75 <221> NAME/KEY: UNSURE
76 <222> LOCATION: (1)..(2)
78 <400> SEQUENCE: 4
W--> 79 Xaa Xaa Leu Lys Asp Ile Thr Arg Arg Leu Lys Ser Ile
      80   1           5           10
      83 <210> SEQ ID NO: 5
      84 <211> LENGTH: 10
      85 <212> TYPE: PRT
      86 <213> ORGANISM: Rattus sp.
      88 <220> FEATURE:
      89 <221> NAME/KEY: UNSURE
      90 <222> LOCATION: (1)..(2)
      92 <400> SEQUENCE: 5
W--> 93 Xaa Xaa Lys Leu Val Arg Pro Pro Val Gln
      94   1           5           10
      97 <210> SEQ ID NO: 6
      98 <211> LENGTH: 10
      99 <212> TYPE: PRT
     100 <213> ORGANISM: Rattus sp.
     102 <220> FEATURE:
     103 <221> NAME/KEY: UNSURE
     104 <222> LOCATION: (1)
     106 <400> SEQUENCE: 6
W--> 107 Xaa Ala His Lys Ser Glu Ile Ala His Arg
      108   1           5           10
      111 <210> SEQ ID NO: 7
      112 <211> LENGTH: 11
      113 <212> TYPE: PRT
      114 <213> ORGANISM: Rattus sp.
      116 <220> FEATURE:
      117 <221> NAME/KEY: UNSURE
      118 <222> LOCATION: (1)
      120 <220> FEATURE:
      121 <221> NAME/KEY: UNSURE
      122 <222> LOCATION: (4)
      123 <223> OTHER INFORMATION: R/L
      125 <400> SEQUENCE: 7
W--> 126 Xaa Pro Ser Xaa Lys Phe Phe Val Gly Gly Asn
      127   1           5           10

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VERIFICATION SUMMARY

DATE: 09/18/2001

PATENT APPLICATION: US/09/419,901

TIME: 16:19:45

Input Set : A:\Ptq-0021.app

Output Set: N:\CRF3\09182001\I419901.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:79 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:93 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7